IN THE SPECIFICATION:

Please replace the paragraph beginning at page 9, line 8 as follows:

--Figure 2 is a representation of the amino acid consensus sequence (SEQ ID NO: 8) from HBV DNA polymerase proteins encompassing regions which are conserved in the RNA polymerase protein. These regions are shown as domains A-E and are underlined. In the consensus sequence the M in the YMDD motif is designated as amino acid number 550. The amino acids which are subject to mutation during 3TC and/or FCV treatment are shown in bold. An asterisk (*) indicates greater than three amino acid possibilities at this position of the consensus sequence. The HbsAg major hydrophilic region containing the neutralization domain is indicated by a double line and the polymerase mutations which alter the HbsAg are indicated in italics.--

Please replace the paragraph beginning at page 9, line 18 as follows:

--Figure 3 is a representation of the nucleotide sequences (SEQ ID NOS: 9-20) from various strains of HBV encoding the surface antigen. The amino acid sequence of the surface antigen beginning at amino acid 108 is shown above the nucleotide sequence.--

Please replace the paragraph beginning at page 9, line 28 as follows:

--Figure 5A is the representation of the nucleotide sequence (SEQ ID NO: 21) of HBV 1.28 genome.--

Please replace the paragraph beginning at page 9, line 30 as follows:

--Figure 5B is the representation of the nucleotide sequence (SEQ ID NO: 22) of HBV 1.5 genome.--

Please replace the paragraph beginning at page 17, line 18 as follows:

--The present invention extends to assaying any HBV mutant carrying a single or multiple substitution, addition and/or deletion or truncation in the amino acid sequence of the catalytic region of the HBV DNA polymerase as compared to the amino acid sequence set forth in Formula I (SEQ ID NO: 5) which is considered herein to define a reference HBV:--

Please replace the paragraph beginning at page 26, line 14 as follows:

--The amino acid sequence of an HBsAg and which is considered to define a reference HBV is set forth below in Formula II (SEQ ID NO: 6):--

Please replace the paragraph beginning at page 33, line 19 as follows:

--The altered HBsAg molecules of the HBV variants of the present invention may also be defined at the nucleotide level. The nucleotide sequence encoding the HBsAg from a reference HBV is set forth below in Formula III (SEQ ID NO: 7):--

Please replace the paragraph beginning at page 43, line 15 as follows:

--Purified recombinant transfer vector and linear AcMNPV baculovirus DNA were co-transfected into Sf21 cells using the BacNBlue transfection kit from Invitrogen (Carlsbad, CA); recombinant viruses were isolated by plaque assay according to the manufacturer's instructions. A series of recombinant viruses were amplified from isolated plaques by infecting 100-mm dishes of Sf21 cells. Viral DNA was extracted from amplified viruses using standard procedures. Purified viral DNA was digested with restriction enzymes and then fractionated by electropyhoresis in a 1.0% v/v agarose gel. Southern blotting was performed to determine which virus isolates contained the intact 1.28, 1.5 or 1.3 HBV construct. A Boehringer Mannheim Random Prime DNA Labeling kit (Indianapolis, IN) was used to generate [P^{32}]-radiolabeled probes. A full-length double-stranded HBV genome was used as a template for all radiolabeled